

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 92.4677
Seconds
(without alignments)
5591.830 Million cell
updates/sec

Title: US-09-300-482-225
Perfect score: 316
Sequence: 1
gataagggtgcgcacactgag.....gaatggagggagtacttcga 316

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:/*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:/*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:/*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:/*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:/*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
